

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/593,859
Source: FRP
Date Processed by STIC: 10/3/86

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 10/03/2006

PATENT APPLICATION: US/10/593,859

TIME: 08:52:50

Input Set : N:\RJAVED\10593859.txt

Output Set: N:\CRF4\10032006\J593859.raw

5 <110> APPLICANT: Lombardo, Dominique
6 Mas, Eric
7 Sadoulet, Marie-Odile
8 Panicot-Dubois, Laurence
9 Bernard, Jean-Paul
12 <120> TITLE OF INVENTION: Glycopeptides derived from pancreatic structures, antibodies
and
13 applications thereof in diagnostics and therapeutics
17 <130> FILE REFERENCE: BKR-107
C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/593,859
C--> 20 <141> CURRENT FILING DATE: 2006-09-22
20 <150> PRIOR APPLICATION NUMBER: FR 04 03378
22 <151> PRIOR FILING DATE: 2004-03-31
26 <150> PRIOR APPLICATION NUMBER: FR 04 13428
28 <151> PRIOR FILING DATE: 2004-12-16
32 <160> NUMBER OF SEQ ID NOS: 14
36 <170> SOFTWARE: PatentIn version 3.1
40 <210> SEQ ID NO: 1
42 <211> LENGTH: 36
44 <212> TYPE: DNA
46 <213> ORGANISM: Homo sapiens
50 <400> SEQUENCE: 1
51 ttcgtaagct tgcgaagctg ggcgccgtgt acagaa 36
54 <210> SEQ ID NO: 2
56 <211> LENGTH: 42
58 <212> TYPE: DNA
60 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 2
65 tttcgtgaat tcacgctaaa acctaatac tgcaggcatc tg 42
68 <210> SEQ ID NO: 3
70 <211> LENGTH: 33
72 <212> TYPE: DNA
74 <213> ORGANISM: Homo sapiens
78 <400> SEQUENCE: 3
79 cgtctaaagc tttttgatgt ctacaccgag tcc 33
82 <210> SEQ ID NO: 4
84 <211> LENGTH: 27
86 <212> TYPE: DNA
88 <213> ORGANISM: Homo sapiens
92 <400> SEQUENCE: 4
93 aaaaagaatt cggagaaaat aatgaat 27
96 <210> SEQ ID NO: 5
98 <211> LENGTH: 28
100 <212> TYPE: DNA

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102 <213> ORGANISM: Homo sapiens
106 <400> SEQUENCE: 5
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110 <210> SEQ ID NO: 6
112 <211> LENGTH: 2350
114 <212> TYPE: DNA
116 <213> ORGANISM: Homo sapiens
120 <220> FEATURE:
122 <221> NAME/KEY: CDS
124 <222> LOCATION: (17)..(2251)
129 <400> SEQUENCE: 6
130 ggccacccag aggctg atg ctc acc atg ggg cgc ctg caa ctg gtt gtg ttg 52
131 Met Leu Thr Met Gly Arg Leu Gln Leu Val Val Leu
132 1 5 10
134 ggc ctc acc tgc tgc tgg gca gtg gcg agt gcc gcg aag ctg ggc gcc 100
135 Gly Leu Thr Cys Cys Trp Ala Val Ala Ser Ala Ala Lys Leu Gly Ala
136 15 20 25
138 gtg tac aca gaa ggt ggg ttc gtg gaa ggc gtc aat aag aag ctc ggc 148
139 Val Tyr Thr Glu Gly Gly Phe Val Glu Gly Val Asn Lys Lys Leu Gly
140 30 35 40
142 ctc ctg ggt gac tct gtg gac atc ttc aag ggc atc ccc ttc gca gct 196
143 Leu Leu Gly Asp Ser Val Asp Ile Phe Lys Gly Ile Pro Phe Ala Ala
144 45 50 55 60
146 ccc acc aag gcc ctg gaa aat cct cag cca cat cct ggc tgg caa ggg 244
147 Pro Thr Lys Ala Leu Glu Asn Pro Gln Pro His Pro Gly Trp Gln Gly
148 65 70 75
150 acc ctg aag gcc aag aac ttc aag aag aga tgc ctg cag gcc acc atc 292
151 Thr Leu Lys Ala Lys Asn Phe Lys Lys Arg Cys Leu Gln Ala Thr Ile
152 80 85 90
154 acc cag gac agc acc tac ggg gat gaa gac tgc ctg tac ctc aac att 340
155 Thr Gln Asp Ser Thr Tyr Gly Asp Glu Asp Cys Leu Tyr Leu Asn Ile
156 95 100 105
158 tgg gtg ccc cag ggc agg aag caa gtc tcc cgg gac ctg ccc gtt atg 388
159 Trp Val Pro Gln Gly Arg Lys Gln Val Ser Arg Asp Leu Pro Val Met
160 110 115 120
162 atc tgg atc tat gga ggc gcc ttc ctc atg ggg tcc ggc cat ggg gcc 436
163 Ile Trp Ile Tyr Gly Gly Ala Phe Leu Met Gly Ser Gly His Gly Ala
164 125 130 135 140
166 aac ttc ctc aac aac tac ctg tat gac ggc gag gag atc gcc aca cgc 484
167 Asn Phe Leu Asn Asn Tyr Leu Tyr Asp Gly Glu Glu Ile Ala Thr Arg
168 145 150 155
170 gga aac gtc atc gtg gtc acc ttc aac tac cgt gtc ggc ccc ctt ggg 532
171 Gly Asn Val Ile Val Val Thr Phe Asn Tyr Arg Val Gly Pro Leu Gly
172 160 165 170
174 ttc ctc agc act ggg gac gcc aat ctg cca ggt aac tat ggc ctt cgg 580
175 Phe Leu Ser Thr Gly Asp Ala Asn Leu Pro Gly Asn Tyr Gly Leu Arg
176 175 180 185
178 gat cag cac atg gcc att gct tgg gtg aag agg aat atc gcg gcc ttc 628
179 Asp Gln His Met Ala Ile Ala Trp Val Lys Arg Asn Ile Ala Ala Phe

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180	190	195	200	
182	ggg ggg gac	ccc aac aac atc acg ctc ttc	ggg gag tct gct gga ggt	676
183	Gly Gly Asp	Pro Asn Asn Ile Thr Leu Phe	Gly Glu Ser Ala Gly Gly	
184	205	210	215	220
186	gcc agc gtc	tct ctg cag acc ctc tcc	ccc tac aac aag ggc ctc atc	724
187	Ala Ser Val	Ser Leu Gln Thr Leu Ser	Pro Tyr Asn Lys Gly Leu Ile	
188		225	230	235
190	cgg cga gcc	atc agc cag agc ggc gtg	gcc ctg agt ccc tgg gtc atc	772
191	Arg Arg Ala	Ile Ser Gln Ser Gly Val	Ala Leu Ser Pro Trp Val Ile	
192		240	245	250
194	cag aaa aac	cca ctc ttc tgg gcc aaa	aag gtg gct gag aag gtg ggt	820
195	Gln Lys Asn	Pro Leu Phe Trp Ala Lys	Lys Val Ala Glu Lys Val Gly	
196		255	260	265
198	tgc cct gtg	ggt gat gcc gcc agg atg	gcc cag tgt ctg aag gtt act	868
199	Cys Pro Val	Gly Asp Ala Ala Arg Met	Ala Gln Cys Leu Lys Val Thr	
200		270	275	280
202	gat ccc cga	gcc ctg acg ctg gcc tat	aag gtg ccg ctg gca ggc ctg	916
203	Asp Pro Arg	Ala Leu Thr Leu Ala Tyr	Lys Val Pro Leu Ala Gly Leu	
204	285	290	295	300
206	gag tac ccc	atg ctg cac tat gtg ggc	ttc gtc cct gtc att gat gga	964
207	Glu Tyr Pro	Met Leu His Tyr Val Gly	Phe Val Pro Val Ile Asp Gly	
208		305	310	315
210	gac ttc atc	ccc gct gac ccg atc aac	ctg tac gcc aac gcc gcc gac	1012
211	Asp Phe Ile	Pro Ala Asp Pro Ile Asn	Leu Tyr Ala Asn Ala Ala Asp	
212		320	325	330
214	atc gac tat	ata gca ggc acc aac aac	atg gac ggc cac atc ttc gcc	1060
215	Ile Asp Tyr	Ile Ala Gly Thr Asn Asn	Met Asp Gly His Ile Phe Ala	
216		335	340	345
218	agc atc gac	atg cct gcc atc aac aag	ggc aac aag aaa gtc acg gag	1108
219	Ser Ile Asp	Met Pro Ala Ile Asn Lys	Gly Asn Lys Lys Val Thr Glu	
220		350	355	360
222	gag gac ttc	tac aag ctg gtc agt gag	ttc aca atc acc aag ggg ctc	1156
223	Glu Asp Phe	Tyr Lys Leu Val Ser Glu	Phe Thr Ile Thr Lys Gly Leu	
224	365	370	375	380
226	aga ggc gcc	aag acg acc ttt gat gtc	tac acc gag tcc tgg gcc cag	1204
227	Arg Gly Ala	Lys Thr Thr Phe Asp Val	Tyr Thr Glu Ser Trp Ala Gln	
228		385	390	395
230	gac cca tcc	cag gag aat aag aag aag	act gtg gtg gac ttt gag acc	1252
231	Asp Pro Ser	Gln Glu Asn Lys Lys Lys	Thr Val Val Asp Phe Glu Thr	
232		400	405	410
234	gat gtc ctc	ttc ctg gtg ccc acc gag	att gcc cta gcc cag cac aga	1300
235	Asp Val Leu	Phe Leu Val Pro Thr Glu	Ile Ala Leu Ala Gln His Arg	
236		415	420	425
238	gcc aat gcc	aag agt gcc aag acc tac	gcc tac ctg ttt tcc cat ccc	1348
239	Ala Asn Ala	Lys Ser Ala Lys Thr Tyr	Ala Tyr Leu Phe Ser His Pro	
240		430	435	440
242	tct cgg atg	ccc gtc tac ccc aaa tgg	gtg ggg gcc gac cat gca gat	1396
243	Ser Arg Met	Pro Val Tyr Pro Lys Trp	Val Gly Ala Asp His Ala Asp	
244	445	450	455	460

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246	gac	att	cag	tac	gtt	ttc	ggg	aag	ccc	ttc	gcc	acc	ccc	acg	ggc	tac	1444
247	Asp	Ile	Gln	Tyr	Val	Phe	Gly	Lys	Pro	Phe	Ala	Thr	Pro	Thr	Gly	Tyr	
248					465					470					475		
250	cgg	ccc	caa	gac	agg	aca	gtc	tct	aag	gcc	atg	atc	gcc	tac	tgg	acc	1492
251	Arg	Pro	Gln	Asp	Arg	Thr	Val	Ser	Lys	Ala	Met	Ile	Ala	Tyr	Trp	Thr	
252					480					485					490		
254	aac	ttt	gcc	aaa	aca	ggg	gac	ccc	aac	atg	ggc	gac	tgc	gct	gtg	ccc	1540
255	Asn	Phe	Ala	Lys	Thr	Gly	Asp	Pro	Asn	Met	Gly	Asp	Ser	Ala	Val	Pro	
256					495					500					505		
258	aca	cac	tgg	gaa	ccc	tac	act	acg	gaa	aac	agc	ggc	tac	ctg	gag	atc	1588
259	Thr	His	Trp	Glu	Pro	Tyr	Thr	Thr	Glu	Asn	Ser	Gly	Tyr	Leu	Glu	Ile	
260					510					515					520		
262	acc	aag	aag	atg	ggc	agc	agc	tcc	atg	aag	cgg	agc	ctg	aga	acc	aac	1636
263	Thr	Lys	Lys	Met	Gly	Ser	Ser	Ser	Met	Lys	Arg	Ser	Leu	Arg	Thr	Asn	
264	525									530					535		540
266	ttc	ctg	cgc	tac	tgg	acc	ctc	acc	tat	ctg	gcg	ctg	ccc	aca	gtg	acc	1684
267	Phe	Leu	Arg	Tyr	Trp	Thr	Leu	Thr	Tyr	Leu	Ala	Leu	Pro	Thr	Val	Thr	
268					545					550					555		
270	gac	cag	gag	gcc	acc	cct	gtg	ccc	ccc	aca	ggg	gac	tcc	gag	gcc	act	1732
271	Asp	Gln	Glu	Ala	Thr	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Glu	Ala	Thr	
272					560					565					570		
274	ccc	gtg	ccc	ccc	acg	ggg	gac	tcc	gag	acc	gcc	ccc	gtg	ccg	ccc	acg	1780
275	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Glu	Thr	Ala	Pro	Val	Pro	Pro	Thr	
276					575					580					585		
278	ggt	gac	tcc	ggg	gcc	ccc	ccc	gtg	ccg	ccc	acg	ggg	gac	tcc	ggg	gcc	1828
279	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	
280					590					595					600		
282	ccc	ccc	gtg	ccg	ccc	acg	ggg	gac	tcc	ggg	gcc	ccc	ccc	gtg	ccg	ccc	1876
283	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Pro	Pro	
284	605									610					615		620
286	acg	ggt	gac	tcc	ggg	gcc	ccc	ccc	gtg	ccg	ccc	acg	ggg	gac	tcc	ggg	1924
287	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	
288					625					630					635		
290	gcc	ccc	ccc	gtg	ccg	ccc	acg	ggg	gac	tcc	ggg	gcc	ccc	ccc	gtg	ccg	1972
291	Ala	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Pro	
292					640					645					650		
294	ccc	acg	ggg	gac	tcc	ggc	gcc	ccc	ccc	gtg	ccg	ccc	acg	ggg	gac	gcc	2020
295	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ala	
296					655					660					665		
298	ggg	ccc	ccc	ccc	gtg	ccg	ccc	acg	ggg	gac	tcc	ggc	gcc	ccc	ccc	gtg	2068
299	Gly	Pro	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	
300					670					675					680		
302	ccg	ccc	acg	ggg	gac	tcc	ggg	gcc	ccc	ccc	gtg	acc	ccc	acg	ggg	gac	2116
303	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Thr	Pro	Thr	Gly	Asp	
304	685									690					695		700
306	tcc	gag	acc	gcc	ccc	gtg	ccg	ccc	acg	ggg	gac	tcc	ggg	gcc	ccc	cct	2164
307	Ser	Glu	Thr	Ala	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	
308					705					710					715		
310	gtg	ccc	ccc	acg	ggg	gac	tct	gag	gct	gcc	cct	gtg	ccc	ccc	aca	gat	2212

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311 Val Pro Pro Thr Gly Asp Ser Glu Ala Ala Pro Val Pro Pro Thr Asp
312          720          725          730
314 gac tcc aag gaa gct cag atg cct gca gtc att agg ttt tagcggtccca      2261
315 Asp Ser Lys Glu Ala Gln Met Pro Ala Val Ile Arg Phe
316          735          740          745
318 tgagccttgg tatcaagagg ccacaagagt gggaccccag gggctcccct cccatcttga      2321
320 gctcttctctg aataaagcct catacccct      2350
323 <210> SEQ ID NO: 7
325 <211> LENGTH: 745
327 <212> TYPE: PRT
329 <213> ORGANISM: Homo sapiens
333 <400> SEQUENCE: 7
335 Met Leu Thr Met Gly Arg Leu Gln Leu Val Val Leu Gly Leu Thr Cys
336 1          5          10          15
339 Cys Trp Ala Val Ala Ser Ala Ala Lys Leu Gly Ala Val Tyr Thr Glu
340          20          25          30
343 Gly Gly Phe Val Glu Gly Val Asn Lys Lys Leu Gly Leu Leu Gly Asp
344          35          40          45
347 Ser Val Asp Ile Phe Lys Gly Ile Pro Phe Ala Ala Pro Thr Lys Ala
348          50          55          60
351 Leu Glu Asn Pro Gln Pro His Pro Gly Trp Gln Gly Thr Leu Lys Ala
352 65          70          75          80
355 Lys Asn Phe Lys Lys Arg Cys Leu Gln Ala Thr Ile Thr Gln Asp Ser
356          85          90          95
359 Thr Tyr Gly Asp Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val Pro Gln
360          100          105          110
363 Gly Arg Lys Gln Val Ser Arg Asp Leu Pro Val Met Ile Trp Ile Tyr
364          115          120          125
367 Gly Gly Ala Phe Leu Met Gly Ser Gly His Gly Ala Asn Phe Leu Asn
368          130          135          140
371 Asn Tyr Leu Tyr Asp Gly Glu Glu Ile Ala Thr Arg Gly Asn Val Ile
372 145          150          155          160
375 Val Val Thr Phe Asn Tyr Arg Val Gly Pro Leu Gly Phe Leu Ser Thr
376          165          170          175
379 Gly Asp Ala Asn Leu Pro Gly Asn Tyr Gly Leu Arg Asp Gln His Met
380          180          185          190
383 Ala Ile Ala Trp Val Lys Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro
384          195          200          205
387 Asn Asn Ile Thr Leu Phe Gly Glu Ser Ala Gly Gly Ala Ser Val Ser
388          210          215          220
391 Leu Gln Thr Leu Ser Pro Tyr Asn Lys Gly Leu Ile Arg Arg Ala Ile
392 225          230          235          240
395 Ser Gln Ser Gly Val Ala Leu Ser Pro Trp Val Ile Gln Lys Asn Pro
396          245          250          255
399 Leu Phe Trp Ala Lys Lys Val Ala Glu Lys Val Gly Cys Pro Val Gly
400          260          265          270
403 Asp Ala Ala Arg Met Ala Gln Cys Leu Lys Val Thr Asp Pro Arg Ala
404          275          280          285
407 Leu Thr Leu Ala Tyr Lys Val Pro Leu Ala Gly Leu Glu Tyr Pro Met

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\RJAVED\10593859.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 3,11 ✓

VERIFICATION SUMMARY

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Input Set : N:\RJAVED\10593859.txt

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L:20 M:270 C: Current Application Number differs, Replaced Current Application No

L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0